

REPLACEMENT SHEET

Figure 1A

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# Aligned_sequences: 2
# 1: Pcan057
# 2: Pcan057v1
# Matrix: EDNAFULL
# Gap_penalty: 100.0
# Extend_penalty: 0.05
=====

Pcan057      1 aaacttcatcaaggtaaggttgcggggtagcggct 50
Pcan057v1    1
Pcan057      51 tgcacacaccttgaagggcttcacccggccctggcttcaggctgg 100
Pcan057v1    1
Pcan057      101 ctgccttnatccgcttatccaatgattggataacggatgagggagtg 150
Pcan057v1   1
Pcan057      151 ggtgccaggtgcttgcggcatggccattcagtcacgctgcagtcct 200
Pcan057v1   1
Pcan057      201 gtcagaaaaatcagtgttattctcattctacatatgagaaaactgagg 250
Pcan057v1   1
Pcan057      251 cttgcagatataaggccaaagttacacagctagtgagtgatgggctg 300
Pcan057v1   1
Pcan057      301 agtttcagactccacagtctcttaaccaccaagcagcatgcccagatg 350
Pcan057v1   1
Pcan057      351 aggtgagaaggaaggagagactgcggccacatgagcatctggacactg 400
Pcan057v1   1
Pcan057      401 catggacaactcactcctccctggctctcgctttgttcttgcgggtg 450
Pcan057v1   1
Pcan057      451 tggtggtggtggactcaaagacggtaaagatagctttctctccctg 500
Pcan057v1   1
Pcan057      501 ggaaatctggggttgttaaaaggcctgctccttttagaaggcagga 550
Pcan057v1   1

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REPLACEMENT SHEET

Figure 1B

Pcan057	551	gggccccaaagggaaagcagaaggtgacagaaggaaagggtcctctgatc	600
Pcan057v1	1		0
Pcan057	601	attgctc----- . .	607
Pcan057v1	1	aattctcgagtcgtcgaccgggtcgacgagctcgagggtcgacgagctcg	50
Pcan057	608	-----	607
Pcan057v1	51	agggcgcgcgcggccggccccacccctcgcagcacccgcgccccgcgccc	100
Pcan057	608	-----	607
Pcan057v1	101	tcccagccgggtccagccggagccatggggccggagccgcagtgagcacc	150
Pcan057	608	-----	607
Pcan057v1	151	atggagctggccgccttgtgccgtggggcttcctcgccctttgcc	200
Pcan057	608	-----	607
Pcan057v1	201	ccccggagccgcgagcacccaagtgtgcacccgcacagacatgaagctgc	250
Pcan057	608	-----	607
Pcan057v1	251	ggctccctgccagtcccgagaccacacctggacatgctccgccacctctac	300
Pcan057	608	-----	607
Pcan057v1	301	cagggctgccaggtggtgcagggaaacctggaactcacctacacctgcccac	350
Pcan057	608	-----	607
Pcan057v1	351	caatgccagcctgtccttcctgcaggatatccaggaggtgcagggctacg	400
Pcan057	608	-----	607
Pcan057v1	401	tgctcatcgctcacaaccaagtgaggcagggtcccactgcagaggctgcgg	450
Pcan057	608	-----	607
Pcan057v1	451	attgtgcgaggcacccagctttgaggacaactatgccctggccgtgct	500
Pcan057	608	-----	607
Pcan057v1	501	agacaatggagacccgctgaacaataccacccctgtcacagggccccc	550

REPLACEMENT SHEET

Figure 1C

Pcan057	608	-----accccacagagatcttggaaa · .	627
Pcan057v1	51	caggaggcctgcggagactgcagcttcgaaggcctcacagagatcttggaaa	600
Pcan057	628	ggaggggtcttgatccagcggAACCCCCAGCTCTGCTACCAAGGACACGAT 	677
Pcan057v1	601	ggaggggtcttgatccagcggAACCCCCAGCTCTGCTACCAAGGACACGAT	650
Pcan057	678	tttgtgaaaggacatctccacaagaacaaccaggctggcttcacactga 	727
Pcan057v1	651	tttgtgaaaggacatctccacaagaacaaccaggctggcttcacactga	700
Pcan057	728	tagacaccaaccgctctcgccctgccACCCCTGTTCTCGATGTGAAG 	777
Pcan057v1	701	tagacaccaaccgctctcgccctgccACCCCTGTTCTCGATGTGAAG	750
Pcan057	778	ggctcccgtgtggggagagaggttctgaggattgtcagagcctgacg 	827
Pcan057v1	751	ggctcccgtgtggggagagaggttctgaggattgtcagagcctgacg	800
Pcan057	828	cactgtctgtgcgggtggctgtgcggcgtgcAAGGGCCACTGCCACTG 	877
Pcan057v1	801	cactgtctgtgcgggtggctgtgcggcgtgcAAGGGCCACTGCCACTG	850
Pcan057	878	actgctgccatgagcagtgtgctgcggctgcACGGGCCCCAAGCACTCT 	927
Pcan057v1	851	actgctgccatgagcagtgtgctgcggctgcACGGGCCCCAAGCACTCT	900
Pcan057	928	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca 	977
Pcan057v1	901	gactgcctggcctgcctccacttcaaccacagtggcatctgtgagctgca	950
Pcan057	978	ctgcccagccctggcacctacaacacacagacacgtttgagtccatgccc 	1027
Pcan057v1	951	ctgcccagccctggcacctacaacacacagacacgtttgagtccatgccc	1000
Pcan057	1028	atcccgagggccggtatatacattcgccgcacgtgtgtgactgcctgtccc 	1077
Pcan057v1	1001	atcccgagggccggtatatacattcgccgcacgtgtgtgactgcctgtccc	1050
Pcan057	1078	tacaactacccctacggacgtggatccctgcacccctgtctgccccct 	1127
Pcan057v1	1051	tacaactacccctacggacgtggatccctgcacccctgtctgccccct	1100
Pcan057	1128	gcacaaccaagaggtgacagcagaggatggaacacacagcggtgtgagaag 	1177
Pcan057v1	1101	gcacaaccaagaggtgacagcagaggatggaacacacagcggtgtgagaag	1150
Pcan057	1178	gcagcaaggccctgtgcggagtgctatggctggcatggagcacttg 	1227
Pcan057v1	1151	gcagcaaggccctgtgcggagtgctatggctggcatggagcacttg	1200

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Figure 1D

Pcan057	1228	cgagaggtgagggcagttaccagtccaaatatccaggagttgctggctg 	1277
Pcan057v1	1201	cgagaggtgagggcagttaccagtccaaatatccaggagttgctggctg 	1250
Pcan057	1278	caagaagatcttgggagcctggcatttcgcggagagcttgatgggg 	1327
Pcan057v1	1251	caagaagatcttgggagcctggcatttcgcggagagcttgatgggg 	1300
Pcan057	1328	acccagcctccaacactgccccgtccagccagagcagctccaagtgtt 	1377
Pcan057v1	1301	acccagcctccaacactgccccgtccagccagagcagctccaagtgtt 	1350
Pcan057	1378	gagactctggaagagatcacaggttacctatacatctcagcatggccgga 	1427
Pcan057v1	1351	gagactctggaagagatcacaggttacctatacatctcagcatggccgga 	1400
Pcan057	1428	cagcctgcctgacctcagcgtttccagaacctgcaagtaatccggggac 	1477
Pcan057v1	1401	cagcctgcctgacctcagcgtttccagaacctgcaagtaatccggggac 	1450
Pcan057	1478	gaattctgcacaatggcgctactcgctgaccctgcaagggtggcattc 	1527
Pcan057v1	1451	gaattctgcacaatggcgctactcgctgaccctgcaagggtggcattc 	1500
Pcan057	1528	agctggctgggctgcgctcactgagggactggcagtggactggccct 	1577
Pcan057v1	1501	agctggctgggctgcgctcactgagggactggcagtggactggccct 	1550
Pcan057	1578	catccaccataacacccacctctgcttcgtgcacacgggtccctgggacc 	1627
Pcan057v1	1551	catccaccataacacccacctctgcttcgtgcacacgggtccctgggacc 	1600
Pcan057	1628	agctttcggaacccgcaccaagctctgctccacactgccaaccggcca 	1677
Pcan057v1	1601	agctttcggaacccgcaccaagctctgctccacactgccaaccggcca 	1650
Pcan057	1678	gaggacgagtgt----- 	1689
Pcan057v1	1651	gaggacgagtgtggtaagacagaggagccagtgctgcgcactccccatctg 	1700
Pcan057	1690	----- 	1689
Pcan057v1	1701	ccagcacacagcagtgccagggggccctggcagcagcggtttggactt 	1750
Pcan057	1690	----- 	1689
Pcan057v1	1751	gtcgagactgcccgtatctgtgcacccttcttgactcagcacagctctgg 	1800
Pcan057	1690	----- 	1689

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Figure 1E

Pcan057v1	1801	ctggcttggcctttggatggcttcttagctgggtccacccgccttg	1850
Pcan057	1690	-----	1689
Pcan057v1	1851	gcatccttcctccccctgtttctgaaatctcagaactttcccttc	1900
Pcan057	1690	-----	1689
Pcan057v1	1901	ctacatcgccccacctgtccccacccctccagcccacagccatgcccac	1950
Pcan057	1690	-----	1689
Pcan057v1	1951	agccagttccctggttcaattggacactggggctccctaaaagtcccct	2000
Pcan057	1690	-----gtgggcgaggggcctggcctggcaccag 	1716
Pcan057v1	2001	gcggtccttccttcactgcagtggcgaggggcctggcctggcaccag	2050
Pcan057	1717	ctgtgcggccgagggcactgctgggtccaggcccacccagtgtgtcaa 	1766
Pcan057v1	2051	ctgtgcggccgagggcactgctgggtccaggcccacccagtgtgtcaa	2100
Pcan057	1767	ctgcagccagttcccttcggggccaggagtgctggaggaatgccgagttac 	1816
Pcan057v1	2101	ctgcagccagttcccttcggggccaggagtgctggaggaatgccgagttac	2150
Pcan057	1817	tgcagggctccccagggagtatgtaatgcaggactgtttggcgtgc 	1866
Pcan057v1	2151	tgcagggctccccagggagtatgtaatgcaggactgtttggcgtgc	2200
Pcan057	1867	caccctgagtgtcagccccagaatggctcagtgacactgtttggaccgga 	1916
Pcan057v1	2201	caccctgagtgtcagccccagaatggctcagtgacactgtttggaccgga	2250
Pcan057	1917	ggctgaccagtgtgtggcctgtgcccactataaggaccctccctctgcg 	1966
Pcan057v1	2251	ggctgaccagtgtgtggcctgtgcccactataaggaccctccctctgcg	2300
Pcan057	1967	tggcccgctgccccagcggtgtgaaacctgacacttcctacatgccatc 	2016
Pcan057v1	2301	tggcccgctgccccagcggtgtgaaacctgacacttcctacatgccatc	2350
Pcan057	2017	tggaagttccagatgaggaggcgcatgccagcctggccatcaactg 	2066
Pcan057v1	2351	tggaagttccagatgaggaggcgcatgccagcctggccatcaactg	2400
Pcan057	2067	caccctcctgtgtggacactggatgacaagggtgtccccccgagcaga 	2116
Pcan057v1	2401	caccctcctgtgtggacactggatgacaagggtgtccccccgagcaga	2450

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Figure 1F

Pcan057	2117	gagccagccctctgacgtccatcatctcgccgtggcattctgctg 	2166
Pcan057v1	2451	gagccagccctctgacgtccatcatctcgccgtggcattctgctg 	2500
Pcan057	2167	gtcgtggtcttgggggtggctttggatcctcatcaagcgacggcagca 	2216
Pcan057v1	2501	gtcgtggtcttgggggtggctttggatcctcatcaagcgacggcagca 	2550
Pcan057	2217	gaagatccggaagtacacgatgcggagactgctgcaggaaacggagctgg 	2266
Pcan057v1	2551	gaagatccggaagtacacgatgcggagactgctgcaggaaacggagctgg 	2600
Pcan057	2267	tggagccgctgacacacctagcggagcgtgccaccaggcgcagatgcgg 	2316
Pcan057v1	2601	tggagccgctgacacacctagcggagcgtgccaccaggcgcagatgcgg 	2650
Pcan057	2317	atcctgaaaagagacggagctgaggaaggtaaggtgcttggatctggcgc 	2366
Pcan057v1	2651	atcctgaaaagagacggagctgaggaaggtaaggtgcttggatctggcgc 	2700
Pcan057	2367	ttttggcacagtcataaggcatctggatccctgatgggagaatgtga 	2416
Pcan057v1	2701	ttttggcacagtcataaggcatctggatccctgatgggagaatgtga 	2750
Pcan057	2417	aaattccagtggccatcaaagtgtttagggaaaacacatccccaaagcc 	2466
Pcan057v1	2751	aaattccagtggccatcaaagtgtttagggaaaacacatccccaaagcc 	2800
Pcan057	2467	aacaaagaaaatcttagacgaagcatacgtgatggctgggtggctcccc 	2516
Pcan057v1	2801	aacaaagaaaatcttagacgaagcatacgtgatggctgggtggctcccc 	2850
Pcan057	2517	atatgtctccgccttctggcatctgcctgacatccacggtgccagctgg 	2566
Pcan057v1	2851	atatgtctccgccttctggcatctgcctgacatccacggtgccagctgg 	2900
Pcan057	2567	tgacacagtttatgcctatggctgccttttagaccatgtccggaaaac 	2616
Pcan057v1	2901	tgacacagtttatgcctatggctgccttttagaccatgtccggaaaac 	2950
Pcan057	2617	cgcggacgcctggctcccaggacctgctgaactggtgtatgcagattgc 	2666
Pcan057v	2951	cgcggacgcctggctcccaggacctgctgaactggtgtatgcagattgc 	3000
Pcan057	2667	caagggatgagctacctggaggatgtgcggctcgtaacacagggacttgg 	2716
Pcan057v1	3001	caagggatgagctacctggaggatgtgcggctcgtaacacagggacttgg 	3050

REPLACEMENT SHEET

Figure 1G

Pcan057	2717	ccgctcggaacgtgctggtaagagtccaaaccatgtcaaaattacagac	2766
Pcan057v1	3051	ccgctcggaacgtgctggtaagagtccaaaccatgtcaaaattacagac	3100
Pcan057	2767	tgcggctggctcggtgtggacattgacgagacagagttaccatgcaga	2816
Pcan057v1	3101	tgcggctggctcggtgtggacattgacgagacagagttaccatgcaga	3150
Pcan057	2817	tggggcaagggtccccatcaagtggatggcgctggagttccattccggcc	2866
Pcan057v1	3151	tggggcaagggtccccatcaagtggatggcgctggagttccattccggcc	3200
Pcan057	2867	ggcggttcacccaccagagtgtgtggagttatgggtgactgtgtgg	2916
Pcan057v1	3201	ggcggttcacccaccagagtgtgtggagttatgggtgactgtgtgg	3250
Pcan057	2917	gagctgatgactttggggcaaacccttacgtggatcccagccggga	2966
Pcan057v1	3251	gagctgatgactttggggcaaacccttacgtggatcccagccggga	3300
Pcan057	2967	gatccctgacctgctggaaaaggggagcggtgtcccgccatct	3016
Pcan057v1	3301	gatccctgacctgctggaaaaggggagcggtgtcccgccatct	3350
Pcan057	3017	gcaccattgatgtctacatgtcatggtaaatgttggatgttactct	3066
Pcan057v1	3351	gcaccattgatgtctacatgtcatggtaaatgttggatgttactct	3400
Pcan057	3067	gaatgtcgccaagattccggagttgggtgtctgaatttcccgatggc	3116
Pcan057v1	3401	gaatgtcgccaagattccggagttgggtgtctgaatttcccgatggc	3450
Pcan057	3117	cagggaccccgagcgcttggatcccgatccagaatgaggacttggcccg	3166
Pcan057v1	3451	cagggaccccgagcgcttggatcccgatccagaatgaggacttggcccg	3500
Pcan057	3167	ccagtcccttggacagcaccttctaccgctactgtggaggacgtgac	3216
Pcan057v1	3501	ccagtcccttggacagcaccttctaccgctactgtggaggacgtgac	3550
Pcan057	3217	atggggacctggatgtggatgtggatctggtaaccaggcaggcgtt	3266
Pcan057v1	3551	atggggacctggatgtggatgtggatctggtaaccaggcaggcgtt	3600
Pcan057	3267	cttctgtccagaccctgccccggcgctggggcatggccaccacaggc	3316
Pcan057v1	3601	cttctgtccagaccctgccccggcgctggggcatggccaccacaggc	3650
Pcan057	3317	accgcagctcatctaccaggagtggcggtgggacctgacactaggcgt	3366
Pcan057v1	3651	accgcagctcatctaccaggagtggcggtgggacctgacactaggcgt	3700

REPLACEMENT SHEET

Figure 1H

Pcan057	3367	gagccctctgaagaggaggccccaggtctccactggcaccctccgaagg	3416
Pcan057v1	3701	gagccctctgaagaggaggccccaggtctccactggcaccctccgaagg	3750
Pcan057	3417	ggctggctccgatgtattgtatggtacactggaaatggggcagccaagg	3466
Pcan057v1	3751	ggctggctccgatgtattgtatggtacactggaaatggggcagccaagg	3800
Pcan057	3467	ggctgcaaaggcctccccacacatgaccccagcccttacagcggtacagt	3516
Pcan057v1	3801	ggctgcaaaggcctccccacacatgaccccagcccttacagcggtacagt	3850
Pcan057	3517	gaggaccccacagtacccctgcacctctgagactgtggctacgttgc	3566
Pcan057v1	3851	gaggaccccacagtacccctgcacctctgagactgtggctacgttgc	3900
Pcan057	3567	cctgacactgcagccccagccctgaatatgtgaaccagccagatgttcggc	3616
Pcan057v1	3901	cctgacactgcagccccagccctgaatatgtgaaccagccagatgttcggc	3950
Pcan057	3617	cccagccccttcgccccgagagggccctgcctgctgcccacactgt	3666
Pcan057v1	3951	cccagccccttcgccccgagagggccctgcctgctgcccacactgt	4000
Pcan057	3667	ggtgccactctggaaaggccaagactctctcccaaggaaatgggt	3716
Pcan057v1	4001	ggtgccactctggaaaggccaagactctctcccaaggaaatgggt	4050
Pcan057	3717	cgtcaaagacgttttgccttgggggtgcgtggagaaccccgagtact	3766
Pcan057v1	4051	cgtcaaagacgttttgccttgggggtgcgtggagaaccccgagtact	4100
Pcan057	3767	tgacaccccagggaggagctgcacctcagccccaccctcctgccttc	3816
Pcan057v1	4101	tgacaccccagggaggagctgcacctcagccccaccctcctgccttc	4150
Pcan057	3817	agcccagcttcgacaaccttattactggaccaggaccaccagcg	3866
Pcan057v1	4151	agcccagcttcgacaaccttattactggaccaggaccaccagcg	4200
Pcan057	3867	gggggctccaccacgcaccccaaaggacacactacggcagagaacccag	3916
Pcan057v1	4201	gggggctccaccacgcaccccaaaggacacactacggcagagaacccag	4250
Pcan057	3917	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	3966
Pcan057v1	4251	agtacctgggtctggacgtgccagtgtgaaccagaaggccaagtccgcag	4300
Pcan057	3967	aagccctgtatgtcctcagggagcagggaaaggcctgacttctgtggca	4016
Pcan057v1	4301	aagccctgtatgtcctcagggagcagggaaaggcctgacttctgtggca	4350

REPLACEMENT SHEET

Figure 1I

Pcan057	4017	tcaagagggtggagggccctccgaccacttcagggaacctgccatgcc 	4066
Pcan057v1	4351	tcaagagggtggagggccctccgaccacttcagggaacctgccatgcc 	4400
Pcan057	4067	aggaacctgtcctaaggAACCTCCTCGTTGAGTCCCAGATGGCT 	4116
Pcan057v1	4401	aggaacctgtcctaaggAACCTCCTCGTTGAGTCCCAGATGGCT 	4450
Pcan057	4117	ggaagggtccagcctcgTTGGAAGAGGAACAGCACTGGGAGTCCTTG 	4166
Pcan057v1	4451	ggaagggtccagcctcgTTGGAAGAGGAACAGCACTGGGAGTCCTTG 	4500
Pcan057	4167	ggattctgaggcccTGCCTGCCAATGAGACTCTAGGGTCCAGTGGATGCCACA 	4216
Pcan057v1	4501	ggattctgaggcccTGCCTGCCAATGAGACTCTAGGGTCCAGTGGATGCCACA 	4550
Pcan057	4217	gccCAGCTTGGCCCTTCCCTCCAGATCCTGGTACTGAAAGCCTTAGGG 	4266
Pcan057v1	4551	gccCAGCTTGGCCCTTCCCTCCAGATCCTGGTACTGAAAGCCTTAGGG 	4600
Pcan057	4267	aagCTGGCCTGAGAGGGGAAGCGGCCCTAACGGAGTGTCTAAGAACAAAA 	4316
Pcan057v1	4601	aagCTGGCCTGAGAGGGGAAGCGGCCCTAACGGAGTGTCTAAGAACAAAA 	4650
Pcan057	4317	gcGACCCATTCAAGAGACTGTCCCTGAAACCTAGTACTGCCCATGAGG 	4366
Pcan057v1	4651	gcGACCCATTCAAGAGACTGTCCCTGAAACCTAGTACTGCCCATGAGG 	4700
Pcan057	4367	aAGGAACAGCAATGGTGTCAGTATCCAGGCTTGTACAGAGTGCTTTCT 	4416
Pcan057v1	4701	aAGGAACAGCAATGGTGTCAGTATCCAGGCTTGTACAGAGTGCTTTCT 	4750
Pcan057	4417	gtttagttttactttttgtttgtttttaaAGATGAAATAAGAC 	4466
Pcan057v1	4751	gtttagttttactttttgtttgtttttaaAGATGAAATAAGAC 	4800
Pcan057	4467	ccAGGGGGAGAAATGGGTGTTGTATGGGGAGGCAAGTGTGGGGGTCCTC 	4516
Pcan057v1	4801	ccAGGGGGAGAAATGGGTGTTGTATGGGGAGGCAAGTGTGGGGGTCCTC 	4850
Pcan057	4517	tccacacccacttgtccattgcaaataatatttgaaaaca 	4559
Pcan057v1	4851	tccacacccacttgtccattgcaaataatatttgaaaaca 	4893

REPLACEMENT SHEET

Figure 2A

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# Aligned_sequences: 2
# 1: Pcan057.aa
# 2: Pcan057v1.aa
# Matrix: EBLOSUM62
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

Pcan057.aa      1                                0
Pcan057v1.aa    1 MELAALCRWGLLALLPPGAASTQVCTGTDMLRLPASPEHLDMLRHLY 50
Pcan057.aa      1                                0
Pcan057v1.aa    51 QGCQVVQGNLELTYLPTNASLSFLQDIQEVEQGYVLIAHNQVRQVPLQRLR 100
Pcan057.aa      1                               MGLSFRLHSLLTTKQ 15
Pcan057v1.aa   101 IVRGQTQLFEDNYALAVLDNGDPLNNTPVTGASPGLRELQLRSL---- 145
Pcan057.aa      16 HAQSRSRGEKEGESCGPHEHLDLAWTTHSSLALALFLLRVWWWDSDKTVKIA 65
Pcan057v1.aa   146 ----- 145
Pcan057.aa      66 FSPPWGIWGLFKRPAPLLEGRRAPREAEGRDRGKGPLIIAHPTEILKGGV 115
Pcan057v1.aa   146 -----TEILKGGV 153
Pcan057.aa      116 LIQRNPQLCYQDTILWKDIFHKNNQLALTLLIDTNRSRACHPCSPMCKGSR 165
Pcan057v1.aa   154 LIQRNPQLCYQDTILWKDIFHKNNQLALTLLIDTNRSRACHPCSPMCKGSR 203
Pcan057.aa      166 CWGESSEDQSLTRVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL 215
Pcan057v1.aa   204 CWGESSEDQSLTRVCAGGCARCKGPLPTDCCHEQCAAGCTGPKHSDCL 253
Pcan057.aa      216 ACLHFNHSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACPYNY 265
Pcan057v1.aa   254 ACLHFNHSGICELHCPALVTYNTDFESMPNPEGRYTFGASCVTACPYNY 303
Pcan057.aa      266 LSTDVGSCTLVCPLHNQEVTAEDEGTQRCEKCSKPCARVCYGLGMEHLREV 315
Pcan057v1.aa   304 LSTDVGSCTLVCPLHNQEVTAEDEGTQRCEKCSKPCARVCYGLGMEHLREV 353
Pcan057.aa      316 RAVTSANIQEFAAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL 365
Pcan057v1.aa   354 RAVTSANIQEFAAGCKKIFGSLAFLPESFDGDPASNTAPLQPEQLQVFETL 403

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REPLACEMENT SHEET

Figure 2B

Pcan057.aa	366	EEITGYLYISAWPDSDLVDFQNLQVIRGRILHNGAYSLTLQGLGISWL 	415
Pcan057v1.aa	404	EEITGYLYISAWPDSDLVDFQNLQVIRGRILHNGAYSLTLQGLGISWL 	453
Pcan057.aa	416	GLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE 	465
Pcan057v1.aa	454	GLRSLRELGSGLALIHHNTHLCFVHTVPWDQLFRNPHQALLHTANRPEDE 	503
Pcan057.aa	466	CVGEGLACHQLCARGHCWGPPTQCVNCSQFLRGQECVEECRVLQGLPRE 	515
Pcan057v1.aa	504	CGKTGSPVCALPICQHTAVPRGPWQQRSWTCADCPSLCTLLDSAQLWLAW	553
Pcan057.aa	516	YVNARHCLPCHPECQPQNGSVTCFGPEADQCVACAHYKDPPFCVARCPSG	565
Pcan057v1.aa	554	PLGMASLAGSYLPWHPSLPLCF	575
Pcan057.aa	566	VKPDLISYMPIWKFPDEEGACQPCPINCTHSCVDLDDKGCPAEQRASPLTS	615
Pcan057v1.aa	576		575
Pcan057.aa	616	IISAVVGILLVVVLGVVFGILIKRRQQKIRKYTMRRLLQETELVEPLTPS	665
Pcan057v1.aa	576		575
Pcan057.aa	666	GAMPNQAQMRLILKETELRKVKVLGGAFGTVYKGIWIPDGENVKIPVAIK	715
Pcan057v1.aa	576		575
Pcan057.aa	716	VLRENTSPKANKEILDEAYVMAGVGSPYVSRLLGICLTSTVQLVTQLMPY	765
Pcan057v1.aa	576		575
Pcan057.aa	766	GCLLDHVRENRGRLGSQDLLNWCMQIAKGMSYLEDVRLVHRDLAARNVLV	815
Pcan057v1.aa	576		575
Pcan057.aa	816	KSPNHVKITDFGLARLLIDIDETEHADGGKVPIKWMALESTILRRRFTHQS	865
Pcan057v1.aa	576		575
Pcan057.aa	866	DVWSYGVTWELMTFGAKPYDGIPAREIPDLLEKGERLPQPPICCIDVYM	915
Pcan057v1.aa	576		575
Pcan057.aa	916	IMVKCWMIDSECRPRFRELVSEFSRMARDPQRFVVIQNEDLGPASPLDST	965
Pcan057v1.aa	576		575
Pcan057.aa	966	FYRSLLEDDDMGDLVDAEYLVPQQGFFCPDPAPGAGGMVHHRHRSSTR	1015

REPLACEMENT SHEET

Figure 2C

Pcan057v1.aa	576	575	
Pcan057.aa	1016	SGGGDLTLGLEPSEEEAPRSPLAPSEGAGSDVFDGLGMGAAKGLQLPT	1065
Pcan057v1.aa	576	575	
Pcan057.aa	1066	HDPSPHQRYSEDPTVPLPSETDGYVAPLTCSPQPEYVNQPDVRPQPPSPR	1115
Pcan057v1.aa	576	575	
Pcan057.aa	1116	EGPLPAARPAGATLERAKTLSPGKNGVVKDVFAGGALENPEYLTPQGGA	1165
Pcan057v1.aa	576	575	
Pcan057.aa	1166	APQPHPPPAFSPAfdnLYWDQDPPERGAPPSTFKGTPTAENPEYLGLDV	1215
Pcan057v1.aa	576	575	
Pcan057.aa	1216	PV	1217
Pcan057v1.aa	576	575	

REPLACEMENT SHEET

Figure 3A

```

# Aligned_sequences: 2
# 1: Pro108
# 2: Pro177
# Matrix: EDNAFULL
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

Pro108      1                               gcacga      6
              ...|...
Pro177      1 gggagggataggacggggagacaaagaagaaaagggtgcggcagcactgccag 50
Pro108      7 gggaaagagggtgatccgaccggggaaaggtcgctggcagggcgagttgg 56
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      51 gggaaagagggtgatccgaccggggaaaggtcgctggcagggcgagttgg 100
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      57 gaaagcggcagccccggccgcccccgccagcccttctccctcccttccc 106
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      101 gaaagcggcagccccggccgcccccgccagcccttctccctcccttccc 150
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      107 acgtccttatctgcctatcgctggaggccaggccgtgcagcatcaagaca 156
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      151 acgtccttatctgcctatcgctggaggccaggccgtgcagcatcaagaca 200
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      157 ggaggaactggaggcattggccggccggggcgccggctcggttta 206
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      201 ggaggaactggaggcattggccggccggggcgccggctcggttta 250
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      207 aataggagctccggctctggctgggacccgaccgctgcggccggctc 256
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      251 aataggagctccggctctggctgggacccgaccgctgcggccggctc 300
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      257 ccgctgctcctgcgggtgatggaaaaccccagccggccggccctgg 306
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      301 ccgctgctcctgcgggtgatggaaaaccccagccggccggccctgg 350
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      307 gcaaggccctctgcgtctctctggccactctggcgccggccggccag 356
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      351 gcaaggccctctgcgtctctctggccactctggcgccggccggccag 400
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      357 cctttggggagagtccatctgttcggccagagccccggccaaatacag 406
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      401 cctttggggagagtccatctgttcggccagagccccggccaaatacag 450
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      407 catcacccacggcaagtggagccagacggcctcccaagcagtacc 456
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro177      451 catcacccacggcaagtggagccagacggcctcccaagcagtacc 500
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |
Pro108      457 ccctgttccggccctgcgcagtggcttcgctgtggggccgcgcatt 506
              ||||| | | | | | | | | | | | | | | | | | | | | | | | | |

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REPLACEMENT SHEET

Figure 3B

Pro177	501	ccctgttccgccccccctgcgcagtggcttcgcgtctggggccgcacat	550
Pro108	507	agctccgactacagcatgtggaggaagaaccaggtaacgtcagtaacggct	556
Pro177	551	agctccgactacagcatgtggaggaagaaccaggtaacgtcagtaacggct	600
Pro108	557	gcgcgactttcgaggcgccggcgaggcctggcgctgtatgaaggagatcg	606
Pro177	601	gcgcgactttcgaggcgccggcgaggcctggcgctgtatgaaggagatcg	650
Pro108	607	aggcggcgggggaggcgctgcagagcgtgcacgcgtgtttcgccccc	656
Pro177	651	aggcggcgggggaggcgctgcagagcgtgcacgcgtgtttcgccccc	700
Pro108	657	gccgtccccagcggcacccggcagacgtcgccggagctggaggtgcagcg	706
Pro177	701	gccgtccccagcggcacccggcagacgtcgccggagctggaggtgcagcg	750
Pro108	707	caggcaactcgctggtctcggtggcgcatcggtcccgccagccccgact	756
Pro177	751	caggcaactcgctggtctcggtggcgcatcggtcccgccagccccgact	800
Pro108	757	ggtcgtggcggtggacagcctggacctgtgcgcacggggaccgttggcgg	806
Pro177	801	ggtcgtggcggtggacagcctggacctgtgcgcacggggaccgttggcgg	850
Pro108	807	gaacaggcggcgctggacacctgttacccctacgcacgcggggacggacagcgg	856
Pro177	851	gaacaggcggcgctggacacctgttacccctacgcacgcggggacggacagcgg	900
Pro108	857	ttcaccttctccatccccaaacttcgcaccatccgcaggacacggta	906
Pro177	901	ttcaccttctccatccccaaacttcgcaccatccgcaggacacggta	950
Pro108	907	ccgagataacgtcctctccatccccaaacttcgcaccatccgcaggacacggta	956
Pro177	951	ccgagataacgtcctctccatccccaaacttcgcaccatccgcaggacacggta	1000
Pro108	957	ccggcgctgaaggccctgcctccatgcgcagggtgacactggtgccgct	1006
Pro177	1001	ccggcgctgaaggccctgcctccatgcgcagggtgacactgctgcggct	1050
Pro108	1007	gcgacagagccccagggcattcatccctccgcggccagtcctgcggca	1056
Pro177	1051	gcgacagagccccagggcattcatccctccgcggccagtcctgcggca	1100
Pro108	1057	gggacaatgagatttagacagcgcct-----	1083
Pro177	1101	gggacaatgagatttagacagcgcctcaggtaacggacatacaggta	1150

REPLACEMENT SHEET

Figure 3C

Pro108	1084	-----	1083
Pro177	1151	atgggacacacacagcagccccgaaccctgccacaggcgaccaccaaacc	1200
Pro108	1084	-----	1083
Pro177	1201	gaacctaaaggctctgagaaattccaagtagggattcgttagtgcgtactgc	1250
Pro108	1084	-----	1083
Pro177	1251	aagatggtcctagaagatttaggattctgttgcattcacacactgaagat	1300
Pro108	1084	-----	1083
Pro177	1301	gtgactcttgcacattatttcagttgaaaggcatcttacaggccacagc	1350
Pro108	1084	-----	1083
Pro177	1351	ccagagggaaagaatgaaaggaggctccagacagtacactgagagacttgt	1400
Pro108	1084	-----	1083
Pro177	1401	cctgtcagacacgcacccacaggtgacactgtgtcacagctgacaagga	1450
Pro108	1084	-----	1083
Pro177	1451	agcttgcattggccctgtgtggccaccgggtgacagctatgcgtcag	1500
Pro108	1084	-----	1083
Pro177	1501	ggcacctgtgggggtctcgggacccagccaccacacagctgggctctg	1550
Pro108	1084	-----	1083
Pro177	1551	ctcacaggcgccctggcctggggcgggcaggtgctgtgatgagcattctcc	1600
Pro108	1084	-----	1083
Pro177	1601	tagctttccaggcacctgctggacagggcaggctggAACGCTGGGCC	1650
Pro108	1084	-----	1083
Pro177	1651	gagtggcagttccctccctactcagctgggtggcagccactggcctcacg	1700
Pro108	1084	-----	1083
Pro177	1701	gagcgccctgtggctggagcgcattgctgggtcgtggcaggcctgtt	1750
Pro108	1084	-----	1083

REPLACEMENT SHEET

Figure 3D

Pro177	1751	ggctctgggtctctgggtctcacatgatatgggtgtggacagtca	gtgt	1800	
Pro108	1084	-----	-----	1083	
Pro177	1801	aggccccagacaacacagcgacttcagactttcccgaggagga	actggagc	1850	
Pro108	1084	-----	-----	1083	
Pro177	1851	ccaccaacctggccatggccccgtcgccctccaccctccatgtt	gctgg	1900	
Pro108	1084	-----	-----	1083	
Pro177	1901	ctggagttgaggcaggtaaaaaaaaaaaaaaaaacacactgc	ccccccaa	gcccatt	1950
Pro108	1084	-----	-----	1083	
Pro177	1951	gtggtagggacagatgtcgcttgaggaggcagcagtaattaca	aggctac	2000	
Pro108	1084	-----	-----	1083	
Pro177	2001	tgtcagccgtcccttggaaagcaaggccaggtcaggcagacagg	aggccg	2050	
Pro108	1084	-----	-----	1083	
Pro177	2051	cctggctggcgaaaaccactccccagacagagactgtgc	ccagtc	ccttggg	2100
Pro108	1084	-----	-----	1083	
Pro177	2101	tccctccatggatgaactggcccttcactcatggccatcggt	gt	2150	
Pro108	1084	-----	-----	1083	
Pro177	2151	gccccctgcccagtgcaggcttggcttcactcatggccacgc	ggat	2200	
Pro108	1084	-----	-----	1083	
Pro177	2201	gccccattccaaggcagatgtccccgagccacttacccaa	caggc	acgt	2250
Pro108	1084	-----	-----	1083	
Pro177	2251	gccagcactgtcggtgtcaactggctggcgaaaagagcc	ccctcg	t	2300
Pro108	1084	-----	-----	1083	
Pro177	2301	ggcagagggtccagagagggtcggtttggccacatgggg	ggcact	ttgg	2350
Pro108	1084	-----	-----	1083	
Pro177	2351	gccacagtggcaggggagcacgtggccagtgc	ccctgggt	ctgccacgt	2400

REPLACEMENT SHEET

Figure 3E

Pro108	1084	-----	1083
Pro177	2401	gtgggagttccaccacaccacaggacttgagcggcagctccggctttacg	2450
Pro108	1084	-----	1083
Pro177	2451	tagaaacgcgcaactccagtccttagttgtgtccgagggttatggtg	2500
Pro108	1084	-----	1083
Pro177	2501	ccatcccatttgcgcactctgcgactgtgcggagaaacgcgaatgc	2550
Pro108	1084	-----	1083
Pro177	2551	ccccgaagggtggcggtggcctctgtatgaatgcacacgttggggaggt	2600
Pro108	1084	-----	1083
Pro177	2601	ggttccgtttgtacgaaggcgctttcacgcgagcggttacacctcggtct	2650
Pro108	1084	-----cagttccagaaacgcgcgtggactgcgaggctcc	1118
Pro177	2651	ccctttgttggccagttccagaaacgcgcgtggactgcgaggctcc	2700
Pro108	1119	ctgtggtcgtcctgggactgtgcggaggccactgtggaggctcgac	1168
Pro177	2701	ctgtggtcgtcctgggactgtgcggaggccactgtggaggctcgac	2750
Pro108	1169	caagagcaggactcgctacgtccgggtccagccgcacaacggagcc	1218
Pro177	2751	caagagcaggactcgctacgtccgggtccagccgcacaacggagcc	2800
Pro108	1219	cctgccccgagctcgaagaagaggctgagtgcgccctgataactgcgtc	1268
Pro177	2801	cctgccccgagctcgaagaagaggctgagtgcgccctgataactgcgtc	2850
Pro108	1269	taagaccagagccccgcagccctgggg-cccccggagccatgggtgtc	1317
Pro177	2851	taagaccagagccccgcagccctggggccccccggagccatgggtgtc	2900
Pro108	1318	gggggctcctgtcaggctcatgctgcaggcgccga-ggcacaggggt	1366
Pro177	2901	gggggctcctgtcaggctcatgctgcaggcgccgaggcacaggggt	2950
Pro108	1367	tgcgcgtgcctgaccgcgggtgaggccgcggcaccatctgcactg	1416
Pro177	2951	tgcgcgtgcctgaccgcgggtgaggccgcggcaccatctgcactg	3000

REPLACEMENT SHEET

Figure 3F

Pro108	1417	aaggccccttgtggccggcacggcattggaaacagcctccctt 	1466
Pro177	3001	aaggccccttgtggccggcacggcattggaaacagcctccctt 	3050
Pro108	1467	cccaaccttgctttagggccccgtgtccgtctgctcagcctcc 	1516
Pro177	3051	cccaaccttgctttagggccccgtgtccgtctgctcagcctcc 	3100
Pro108	1517	tcctcctgcaggataaaagtcatccccaggctccagctactctaaattat 	1566
Pro177	3101	tcctcctgcaggataaaagtcatccccaggctccagctactctaaattat 	3150
Pro108	1567	ggtctccttataagttattgtgtccaggagattgtccttcatcgcca 	1616
Pro177	3151	-gtctccttataagttattgtgtccaggagattgtccttcatcgcca 	3199
Pro108	1617	ggggcctggctccacgtggttgcagataacctcagacctggtgctctagg 	1666
Pro177	3200	ggggcctggctccacgtggttgcagataacctcagacctggtgctctagg 	3249
Pro108	1667	ctgtgctgagcccactctcccgaggcgcatccaagggggccacttga 	1716
Pro177	3250	ctgtgctgagcccactctcccgaggcgcatccaagggggccacttga 	3299
Pro108	1717	gaagtgaataaatggggcggttgcgaagcgtaagtgtttccatgttatg 	1766
Pro177	3300	gaagtgaataaatggggcggttgcgaagcgtaagtgtttccatgttatg 	3349
Pro108	1767	gatctctctgcgttgaataaagactatctgttgctcac . .	1807
Pro177	3350	gatctctctgcgttgaataaagactatctgttgctcaaaaa . .	3393

REPLACEMENT SHEET

Figure 4

```
Aligned_sequences: 2
# 1: PRO108.aa
# 2: PRO177.aa
# Matrix: EBLOSUM62
# Gap_penalty: 100.0
# Extend_penalty: 0.01
#=====

PRO108.aa      1 MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGK      50
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa      1 MENPSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGK      50
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
PRO108.aa      51 WSQTAFFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFEAER  100
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa      51 WSQTAFFPKQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFEAER  100
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
PRO108.aa     101 GEAWALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVS  150
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa     101 GEAWALMKEIEAAGEALQSVHEVFSAPAVPSGTGQTSAELEVQRRHSLVS  150
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | |
PRO108.aa    151 FVVRIVPSPDWFGVGVDSLDCDGDRWREQAALDLYPYDAGTDSGFTFSSP  200
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa    151 FVVRIVPSPDWFGVGVDSLDCDGDRWREQAALDLYPYDAGTDSGFTFSSP  200
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | |
PRO108.aa    201 NFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSPRA  250
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa    201 NFATIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLRQSPRA   250
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | |
PRO108.aa    251 FIPPAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKS  300
                 ||||||| | | | | | | | | | | | | | | | | | | | | | | | | |
PRO177.aa    251 FIPPAPVLPSRDNEIVDSASGNGHTGHMGHTAAPNPATGRPPNPNLRL  298
                 | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. | .. |
PRO108.aa    301 RTRYVRVQPANNGSPCPELEEEAECVPDNCV      331
PRO177.aa    299
```

REPLACEMENT SHEET

Figure 5A

```

# Aligned_sequences: 2
# 1: PRO108.aa
# 2: PRO177.orf
# Matrix: EBLOSUM62
# Gap_penalty: 100.0
# Extend_penalty: 0.01
=====

PRO108.aa      1                                0
PRO177.orf     1 RCDSCTLFAVESILQGHSPEERMKGGSRQYLRDSVLSDTHPQVTCVSQLT 50
PRO108.aa      1                                0
PRO177.orf     51 RKLARMALCGHRVTAMLQGTCGLGTQPPHSSGLCSQAPWPGAGQVLMSI 100
PRO108.aa      1                                0
PRO177.orf    101 LLALPGTCWTGQAGNAGAEWFPPYSAGWQPLASRSACGLERIAGSWVRA 150
PRO108.aa      1                                0
PRO177.orf    151 CWLWVSGSHLIWVWDSQCRPQTADFRLSRGGTGAHPGPGRRPPPSML 200
PRO108.aa      1                                0
PRO177.orf    201 LAGVEAGTGPPHTCPPSHVVGTDVVLRSSSNYKLTVSRPWKQGPQVRQE 250
PRO108.aa      1                                0
PRO177.orf    251 AAWLAGTTPQTEVPSPGSLLIWDELGLPVPASVLPLPSAGLGSSLICPR 300
PRO108.aa      1                                0
PRO177.orf    301 GCPIPSRCPRATYPTGRRASTVRGVQLVWREEPLVGRGSREVRFAPHLG 350
PRO108.aa      1                                0
PRO177.orf    351 LGHSGQGSTWPVPWVCHDVGVPPPQGLERQLLLRNAQLQSLGCVRGCY 400
PRO108.aa      1                                MEN      3
                                                . . .
PRO177.orf    401 GAIPSCRSLCDCAEKRKCPRRVGVASDECTRWWEVASVCTKRLFRAFTS 450
PRO108.aa      4 PSPAAALGKALCALLLATLGAAGQPLGGESICSARAPAKYSITFTGKWSQ 53
                                                . | | ..
PRO177.orf    451 VSPLL----- 455
PRO108.aa      54 TAFTPQYPLFRPPAQWSSLLGAAHSSDYSMWRKNQYVSNGLRDFAERGEA 103

```

REPLACEMENT SHEET

Figure 5B

PRO177.orf	456	-----	455
PRO108.aa	104	WALMKEIEAAGEALQSVHAVFSAPAVPSGTGQTSAELEVQRRHSLVSFVV	153
PRO177.orf	456	-----	455
PRO108.aa	154	RIVPSPDWVFVGVDSDLCDGDRWREQAALDLYPYDAGTDSGFTFSSPNFA	203
PRO177.orf	456	-----	455
PRO108.aa	204	TIPQDTVTEITSSSPSHPANSFYYPRLKALPPIARVTLVRLRQSRAFIP	253
PRO177.orf	456	-----	455
PRO108.aa	254	PAPVLPSRDNEIVDSASVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRT ..	303
PRO177.orf	456	-----GPVPETPLDCEVSLWSSWGLCGGHCGRLGTKSRT	490
PRO108.aa	304	YVRVQPANNGSPCPELEEEAECVPDNCV 	331
PRO177.orf	491	YVRVQPANNGSPCPELEEEAECVPDNCV	518